

FIGURE 1

1	ATGTCAGTGGGAGCCATGAAGAAGGGAGTGGGGAGGGCAGTTGGGCTTGGAGCGGCAGC	60
61	GGCTGCCAGGCTACGGAGGAAGACCCCTTCCCGACTGCGGGGCTTGGCTCCGGGACAA	120
121	GGTGGCAGCGCTGGAGGCTGCCCGCAGCCTGCGTGGGTGGAGGGAGCTCAGCTCGGTTG	180
181	TGGGAGCAGCGCAGCCGCACTGGCTGGATGGACCTGGAAGCCTCGCTGCTGCCCACTGGT	240
241	CCCAATGCCAGCAACACCTCTGATGGCCCCGATAACCTCACTTCAGCAGGATCACCTCCT	300
301	CGCAGGGGAGCATCTCCTACATCAACATCATCATGCCCTTCGGTGTTCGGCACCATCTGC	360
361	CTCCTGGGCATCATCGGGAACCTCCACGGTCATCTTCGGGTCGTGAAGAAGTCCAAGCTG	420
421	CACCTGGTGCAACAACGTCCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCCTC	480
481	TTTCTCCTGGGCATGCCCTTTCATGATCCACCAGCTCATGGGCAATGGGTGTGGCACTTT	540
541	GGGAGACCATGTGCACCCCTCATCACGGCCATGGATGCCAATAGTCAGTTCACCAAGCACC	600
601	TACATCCTGACCGCCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCTCC	660
661	ACGAAGTTCGGGAAGCCCTCTGTGGCCACCCCTGGTGATCTGCCCTCCTGTGGGCCCTCTCC	720
721	TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCCAGGAGGTGCA	780
781	GTGGGCTGCCGCATACGCCCTGCCCAACCCAGACACTGACCTCTACTGGTTCACCCCTGTAC	840
841	CAGTTTTCCTGGCCCTTTGGCCCTGCCCTTTTGTGTCTATCACAGCCGCATACGTGAGGATC	900
901	CTGCAGCGCATGACGTCCCTCAGTGGCCCCCGCCTCCAGCGCAGCATCCGGCTGCCGACA	960
961	AAGAGGGTGACCCGCACAGCCATCGCCCATCTGTCTGGTCTTCTTTGTGTGTGGCACCC	1020
1021	TACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCCCGACCCCTCACCTTTGTCTAC	1080
1081	TTATACAATGCGGCCATCAGCTTGGGCTATGCCAACAGCTGCCCTCAACCCCTTTGTGTAC	1140
1141	ATCGTGCTCTGTGAGACGTTCCGCAACGCTTGGTCTGTGGTGAAGCCTGCCAGCCAG	1200
1201	GGCAGCTTCGGCTGTCAAGCAACGCTCAGACGGCTGACGAGGAGGACAGAAAGCACA	1260
1261	GGCACCTGA	1269

2/27

FIGURE 2

1	M	S	V	G	A	M	K	K	G	V	G	R	A	V	G	L	G	G	G	S	20
21	G	C	Q	A	T	E	E	D	P	L	P	D	C	G	A	C	A	P	G	Q	40
41	G	G	R	R	W	R	L	P	Q	P	A	W	V	E	G	S	S	A	R	L	60
61	W	E	Q	A	T	G	T	G	W	M	D	L	E	A	S	L	L	P	T	G	80
81	P	N	A	S	N	T	S	D	G	P	D	N	L	T	S	A	G	S	P	P	100
101	R	T	G	S	I	S	Y	I	N	I	I	M	P	S	V	F	G	T	I	C	120
121	L	L	G	I	I	G	N	S	T	V	I	F	A	V	V	K	K	S	K	L	140
141	H	W	C	N	N	V	P	D	I	F	I	I	N	L	S	V	V	D	L	L	160
161	F	L	L	G	M	P	F	M	I	H	Q	L	M	G	N	G	V	W	H	F	180
181	G	E	T	M	C	T	L	I	T	A	M	D	A	N	S	Q	F	T	S	T	200
201	Y	I	L	T	A	M	A	I	D	R	Y	L	A	T	V	H	P	I	S	S	220
221	T	K	F	R	K	P	S	V	A	T	L	V	I	C	L	L	W	A	L	S	240
241	F	I	S	I	T	P	V	W	L	Y	A	R	L	I	P	F	P	G	G	A	260
261	V	G	C	G	I	R	L	P	N	P	D	T	D	L	Y	W	F	T	L	Y	280
281	Q	F	F	L	A	F	A	L	P	F	V	V	I	T	A	A	Y	V	R	I	300
301	L	Q	R	M	T	S	S	V	A	P	A	S	Q	R	S	I	R	L	R	T	320
321	K	R	V	T	R	T	A	I	A	I	C	L	V	F	F	V	C	W	A	P	340
341	Y	Y	V	L	Q	L	T	Q	L	S	I	S	R	P	T	L	T	F	V	Y	360
361	L	Y	N	A	A	I	S	L	G	Y	A	N	S	C	L	N	P	F	V	Y	380
381	I	V	L	C	E	T	F	R	K	R	L	V	L	S	V	K	P	A	A	Q	400
401	G	Q	L	R	A	V	S	N	A	Q	T	A	D	E	E	R	T	E	S	K	420
421	G	T																		422	

10029314-12001

3/27

FIGURE 3

1	M S V G A M K K G V G R A V G L G G G S	20
21	G C Q A T E E D P L P D C G A C A P G Q	40
41	G G R R W R L P Q P A W V E G S S A R L	60
61	W E Q A T G T G W M D L E A S L L P T G	80
81	P N A S N T S D G P D N L T S A G S P P	100
101	R T G S I S Y I N <u>I I M P S V F G T I C</u>	120
121	<u>L L G I I G N S T V I F A V V K K S K L</u>	140
141	H W C N N V P D <u>I F I I N L S V V D L L</u>	160
161	<u>F L L G M P F M I H Q L M G N G V W H F</u>	180
181	G E T M C T L I T A M D <u>A N S O F T S T</u>	200
201	<u>Y I L T A M A I D R Y L A T V H P I S S</u>	220
221	T K F R K P S <u>V A T L V I C L L W A L S</u>	240
241	<u>F I S I T P V W L Y A R L I P F P G G A</u>	260
261	<u>V G C G I R L P N P D T D L Y W F T L Y</u>	280
281	<u>Q F F L A F A L P F V V I T A A Y V R I</u>	300
301	<u>L Q R M T S S V A P A S Q R S I R L R T</u>	320
321	K R <u>V T R T A I A I C L V F F V C W A P</u>	340
341	<u>Y Y V L O L T O L S I S R P T L T F V Y</u>	360
361	<u>L Y N A A I S L G Y A N S C L N P F V Y</u>	380
381	<u>I V L C E T F R K R L V L S V K P A A Q</u>	400
401	G Q L R A V S N A Q T A D E E R T E S K	420
421	G T	422

FIGURE 4

1 GCAGGGACCTGCACCGGCTGCATGGATCTGCAAACCTCGTTGCTGTCCACTGGCCCCAA 60
 61 TGCCAGCAACATCTCCGATGGCCAGGATAATCTCACATTGCCGGGTACCTCCTCGCAC 120
 121 AGGAGTGTCTCCTACATCAACATCATATATGCCCTTCCGCTGTTGGTACCATCTGTCTCCT 180
 181 GGGCATCGTGGGAAACTCCACGGTCATCTTTGCTGTGGTGAAGAAGTCCAAGCTACACTG 240
 241 GTGCAGCAACGTCCCCGACATCTTCATCATCAACCTCTCTGTGGTGGATCTGCTCTTCCT 300
 301 GCTGGGCATGCCCTTTTCATGATCCACAGCTCATGGGGAACGGCGTCTGGCACTTTGGGA 360
 361 AACCATGTGCACCCCTCATCACAGCCATGGACGCCAACAGTCAGTTCACTAGCACCTACAT 420
 421 CCTGACTGCCATGACCATTGACCGCTACTTGGCCACCGTCCACCCCATCTCCTCCACCAA 480
 481 GTTCCGGAAGCCCTCCATGGCCACCCCTGGTGATCTGCCCTCCTGTGGGGCTCTCCTTCAT 540
 541 CAGTATCACCCCTGTGTGGCTCTACGCCAGGCTCATTCCTTCCCAGGGGTGCTGTGGG 600
 601 CTGTGGCATCCGCCCTGCCAAACCCGGACACTGACCTCTACTGGTTCACCTCTGTACCAGTT 660
 661 TTTCCCTGGCCCTTTGCCCTTCCGTTTGTGGTCATTACCGCCGCATACGTGAAATACTACA 720
 721 GCGCATGACGCTTTCGGTGGCCCCAGCCTCCCAACGCAGCATCCGGCTTCGGACAAAGAG 780
 781 GGTGACCCGCACGGCCATTGCCATCTGTCTGGTCTTCTTGTGTGCTGGGCACCCCTACTA 840
 841 TGTGCTGCAGCTGACCCAGCTGTCCATCAGCCGCCGCCACCTCACGTTTGTCTACTTGTGA 900
 901 CAACGGGCCATCAGCTTGGGCTATGCTAACAGCTGCCCTGAACCCCTTTGTGTACATAGT 960
 961 GCTCTGTGAGACCTTTCGAAACCGCTTGGTGTGTGTCAGTGAAGCCTGCAGCCCCAGGGCA 1020
 1021 GCTCCGCACGGTCAAGCAACGCTCAGACAGCTGATGAGGAGAGGACAGAAAGCAAGGCAC 1080
 1081 CTGACAATTCCCCAGTCGCCCTCCAAGTCAGGCCACCCCATCAAAACCGTGGGGAGAGATAC 1140
 1141 TGAGATTAAACCCCAAGGCTACCCCTGGGAGAATGCAGAGGCTGGAGGCTGGGGGCTGTAG 1200
 1201 CAACACATTCAC

FIGURE 5

1	M	D	L	Q	L	T	S	L	V	V	S	L	P	F	K	V	V	G	Q	H	L	F	W	A	I	P	Y	A	S	F	T	L	N	K	R		20
21	Q	D	N	L	P	T	S	L	V	V	S	L	P	F	K	V	V	G	Q	H	L	F	W	A	I	P	Y	A	S	F	T	L	N	K	R		40
41	I	I	M	F	A	T	S	L	V	V	S	L	P	F	K	V	V	G	Q	H	L	F	W	A	I	P	Y	A	S	F	T	L	N	K	R		60
61	V	I	I	N	M	S	L	V	V	S	L	P	F	K	V	V	G	Q	H	L	F	W	A	I	P	Y	A	S	F	T	L	N	K	R		80	
81	F	I	I	L	A	N	S	L	V	V	S	L	P	F	K	V	V	G	Q	H	L	F	W	A	I	P	Y	A	S	F	T	L	N	K	R		100
101	H	Q	M	D	A	T	S	L	V	V	S	L	P	F	K	V	V	G	Q	H	L	F	W	A	I	P	Y	A	S	F	T	L	N	K	R		120
121	A	R	L	V	I	C	L	P	Y	A	S	L	P	F	K	V	V	G	Q	H	L	F	W	A	I	P	Y	A	S	F	T	L	N	K	R		140
141	R	Y	L	A	R	I	L	D	I	T	R	F	P	V	S	L	V	I	C	L	P	Y	A	S	L	P	Y	A	S	F	T	L	N	K	R		160
161	T	Y	A	R	T	I	L	D	I	T	R	F	P	V	S	L	V	I	C	L	P	Y	A	S	L	P	Y	A	S	F	T	L	N	K	R		180
181	Y	A	R	T	I	L	D	I	T	R	F	P	V	S	L	V	I	C	L	P	Y	A	S	L	P	Y	A	S	F	T	L	N	K	R		200	
201	P	F	V	S	L	V	I	C	L	P	Y	A	S	L	V	I	C	L	P	Y	A	S	L	P	Y	A	S	F	T	L	N	K	R		220		
221	F	P	A	S	L	V	I	C	L	P	Y	A	S	L	V	I	C	L	P	Y	A	S	L	P	Y	A	S	F	T	L	N	K	R		240		
241	P	I	C	L	V	R	F	P	T	L	N	K	R																							260	
261	I	S	I	S	R	S	C	L	V	R	F	P	T	L	N	K	R																			280	
281	S	Y	A	N	S	C	L	V	R	F	P	T	L	N	K	R																				300	
301	Y	A	N	S	C	L	V	R	F	P	T	L	N	K	R																					320	
321	R	L	V	L	S	E																													340		
341	Q	T	A																																354		

FIGURE 6

IP release in MCH1- and
mock-transfected Cos-7 cells

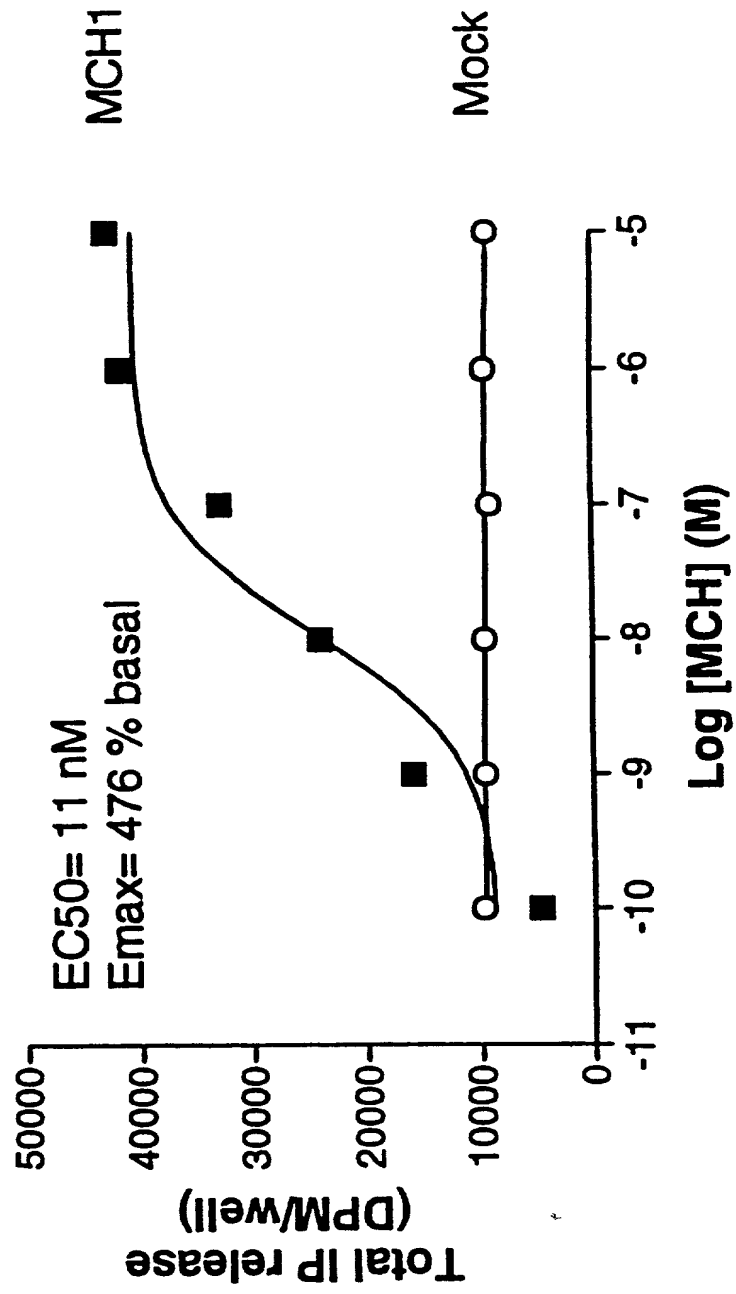
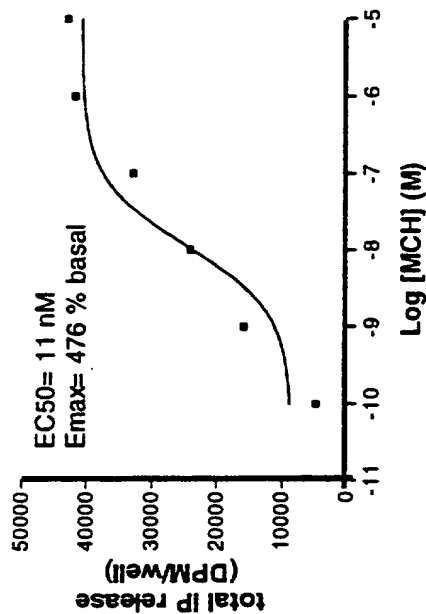
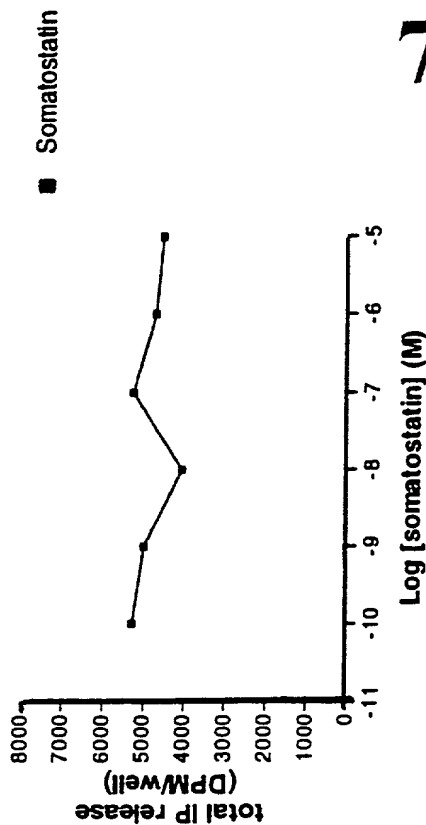


FIGURE 7

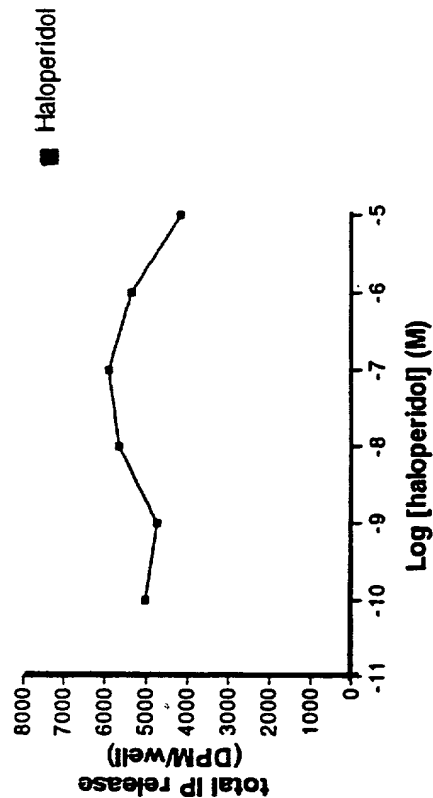
IP release in MCH1-transfected
Cos-7 cells
24 well, 10/9/98



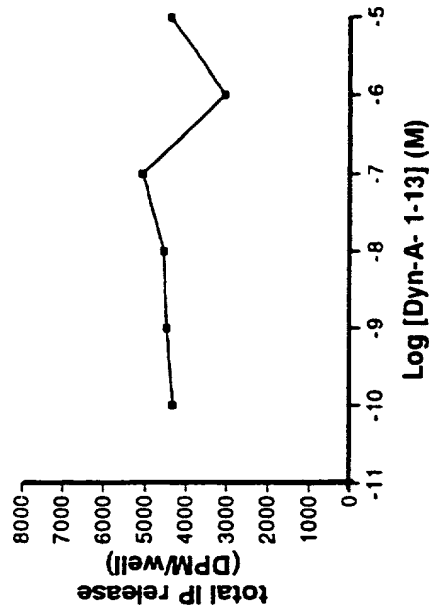
IP release in MCH1-transfected
Cos-7 cells
24 well, 10/9/98



IP release in MCH1-transfected
Cos-7 cells
24 well, 10/9/98



IP release in MCH1-transfected
Cos-7 cells
24 well, 10/9/98

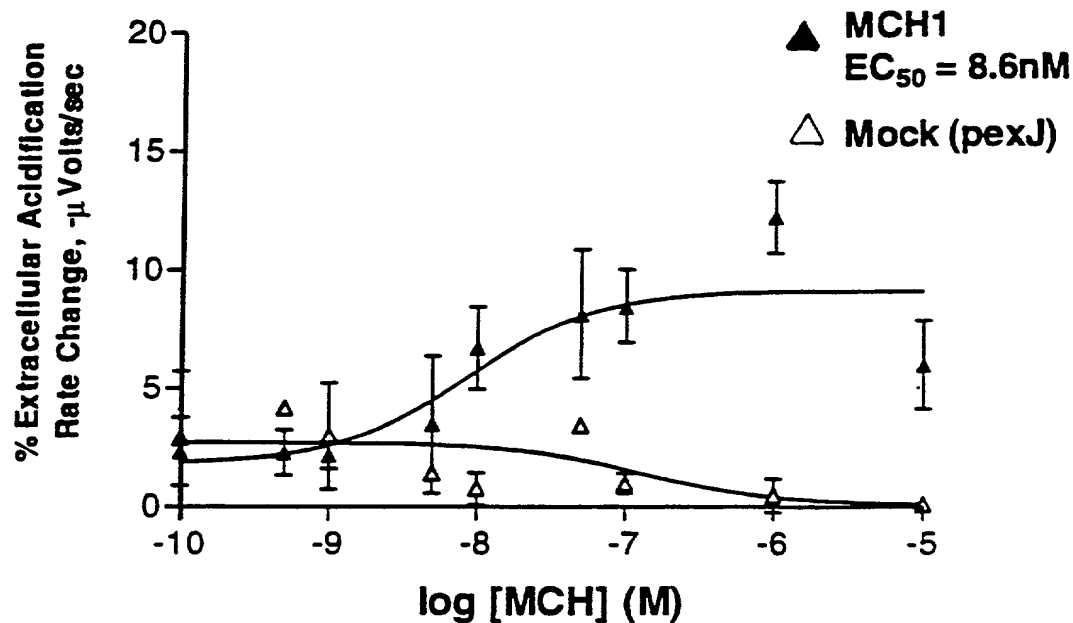


7/27

FIGURE 8

8/27

Microphysiometer Response
CHO cells



Microphysiometer Response
CHO cells

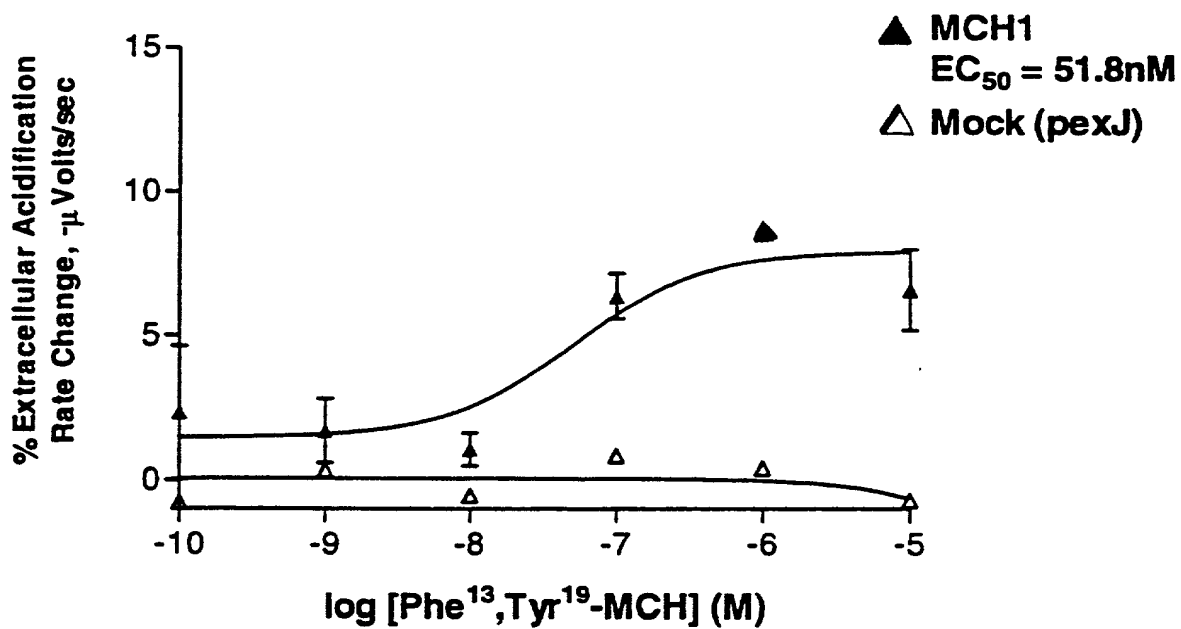
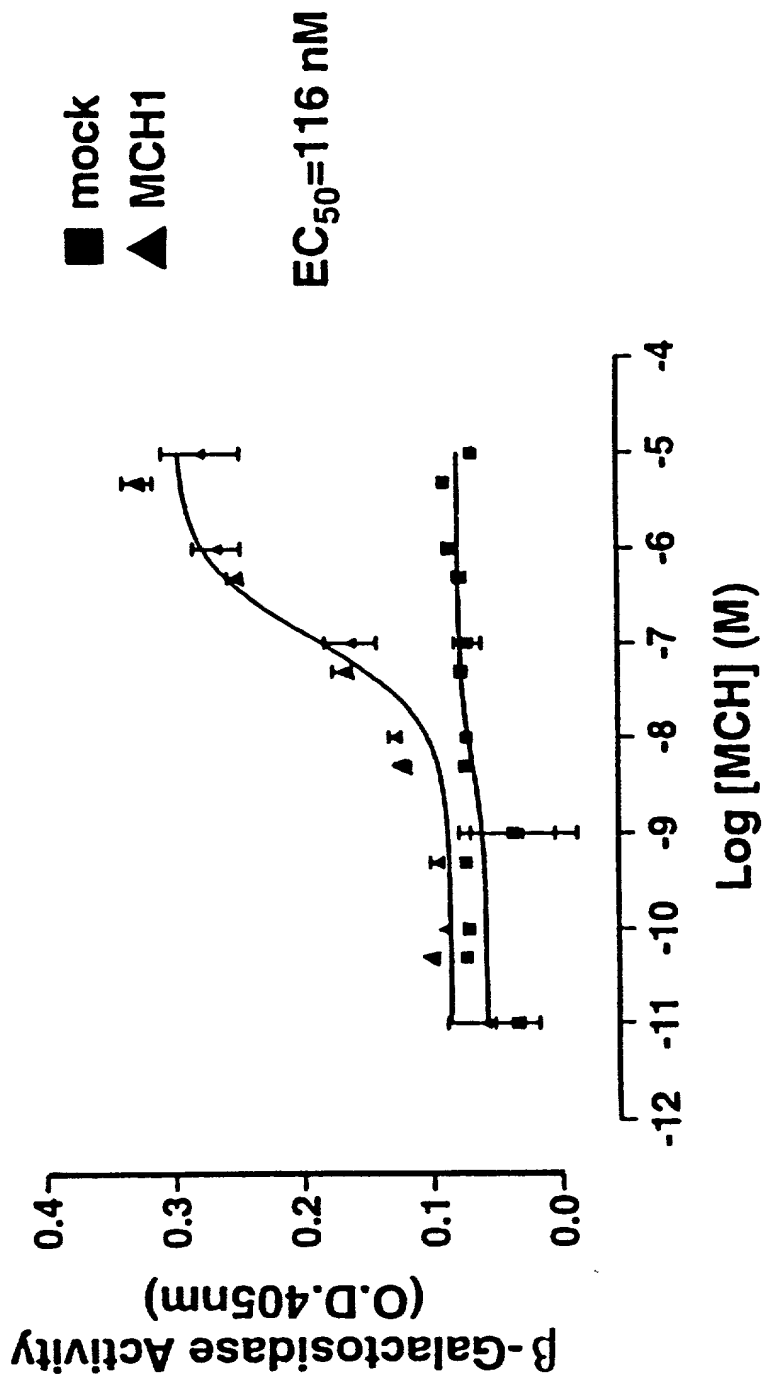


FIGURE 9

Agonist-Mediated c-fos- β -gal Activity in Cos-7 Cells

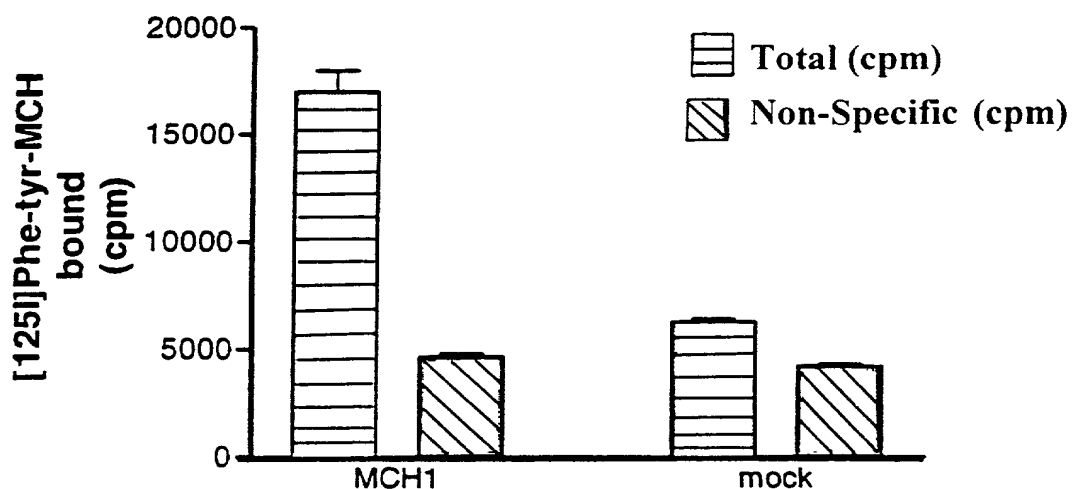


9/27

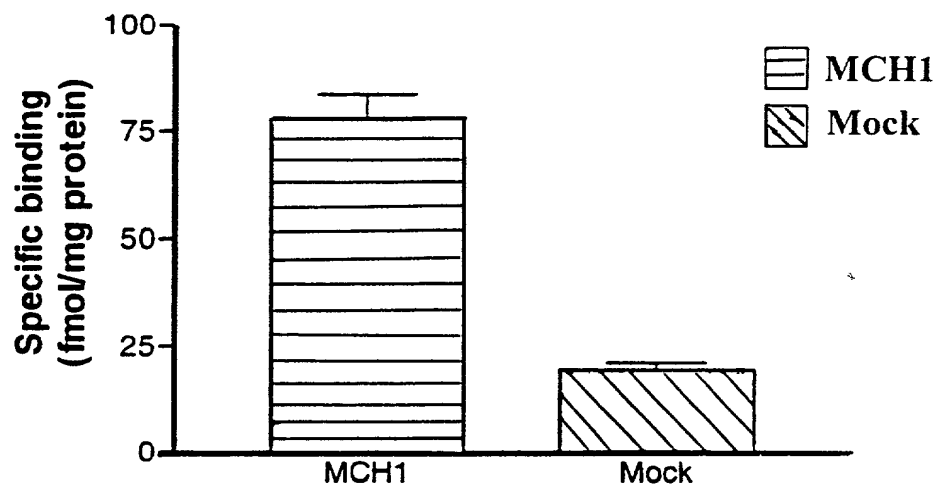
10/27

FIGURE 10

**[¹²⁵I]Phe13-Tyr19-MCH
binding on transiently
transfected Cos-7 cells**

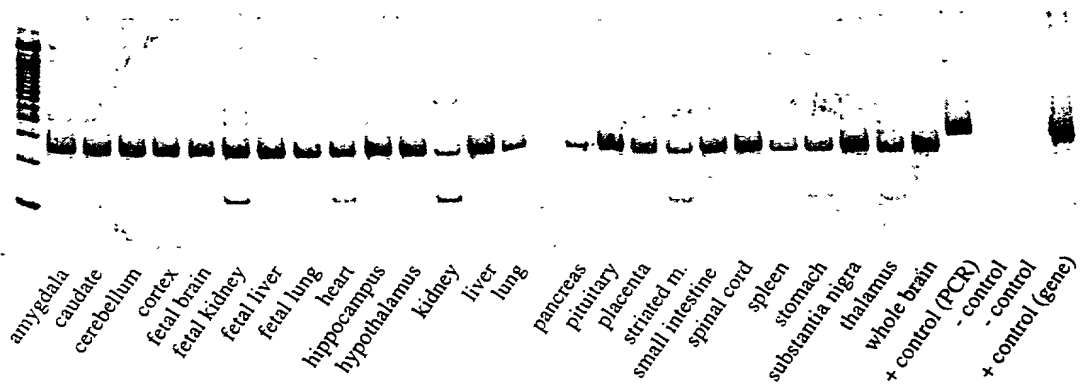


**[¹²⁵I]Phe13-Tyr19-MCH
binding on transiently
transfected Cos-7 cells**



11/27

FIGURE 11



10069314-12001

FIGURE 12

TL231	1	MSVGAMKKGV	GRAVGLGGGS	GCQATEEDPL	PDCGACA?GQ	40
R106		MSVGAMKKGV	GRAVGLGGGS	GCQATEEDPL	PDCGACA?GQ	
R114		MSVGAaKKGV	GRAVGLGGGS	GCQATEEDPL	PDCGACA?GQ	
BO120		~~~~~	~~~~~	~~~~~	~~~~~	

TL231	41	GRRRWRLPQ?	AWVEGSSARL	WEQATGTGWM	DLEASLLPTG	80
R106		GRRRWRLPQ?	AWVEGSSARL	WEQATGTGwa	DLEASLLPTG	
R114		GRRRWRLPQ?	AWVEGSSARL	WEQATGTGwa	DLEASLLPTG	
BO120		~~~~~	~~~~~	~~~~~M	DLEASLLPTG	

TL231	81	PNASNTSDG?	DNLTSA?GSP?	100
R106		PNASNTSDG?	DNLTSA?GSP?	
R114		PNASNTSDG?	DNLTSA?GSP?	
BO120		PNASNTSDG?	DNLTSA?GSP?	

13/27

FIGURE 13

1	M	S	V	G	A	M	K	K	G	V	G	R	A	V	G	L	G	G	G	S	20
21	G	C	Q	A	T	E	E	D	P	L	P	D	C	G	A	C	A	P	G	Q	40
41	G	G	R	R	W	R	L	P	Q	P	A	W	V	E	G	S	S	A	R	L	60
61	W	E	Q	A	T	G	T	G	W	A	D	L	E	A	S	S	L	P	T	G	80
81	P	N	A	S	N	T	S	D	G	P	D	N	L	T	S	A	G	S	P	P	100
101	R	T	G	S	I	S	Y	I	N	I	I	M	P	S	V	F	G	T	I	C	120
121	L	L	G	I	I	G	N	S	T	V	I	F	A	V	V	K	K	S	K	L	140
141	H	W	C	N	N	V	P	D	I	F	I	I	N	L	S	V	V	D	L	L	160
161	F	L	L	G	M	P	F	M	I	H	Q	L	M	G	N	G	V	W	H	F	180
181	G	E	T	M	C	T	L	I	T	A	M	D	A	N	S	Q	F	T	S	T	200
201	Y	I	L	T	A	M	A	I	D	R	Y	L	A	T	V	H	P	I	S	S	220
221	T	K	F	R	K	P	S	V	A	T	L	V	I	C	L	L	W	A	L	S	240
241	F	I	S	I	T	P	V	W	L	Y	A	R	L	I	P	F	P	G	G	A	260
261	V	G	C	G	I	R	L	P	N	P	D	T	D	L	Y	W	F	T	L	Y	280
281	Q	F	F	L	A	F	A	L	F	F	V	V	I	T	A	A	Y	V	R	I	300
301	L	Q	R	M	T	S	S	V	A	P	A	S	Q	R	S	I	R	L	R	T	320
321	K	R	V	T	R	T	A	I	A	I	C	L	V	F	F	V	C	W	A	P	340
341	Y	Y	V	L	Q	L	T	Q	L	S	I	S	R	P	T	L	T	F	V	Y	360
361	L	Y	N	A	A	I	S	L	G	Y	A	N	S	C	L	N	P	F	V	Y	380
381	I	V	L	C	E	T	F	R	K	R	L	V	L	S	V	K	P	A	A	Q	400
401	G	Q	L	R	A	V	S	N	A	Q	T	A	D	E	E	R	T	E	S	K	420
421	G	?																		422	

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14/27

FIGURE 14

1	M	S	V	G	A	A	K	K	G	V	G	R	A	V	G	L	G	G	G	S	20
21	G	C	Q	A	T	E	E	D	P	L	P	D	C	G	A	C	A	P	G	Q	40
41	G	G	R	R	W	R	L	P	Q	P	A	W	V	E	G	S	S	A	R	L	60
61	W	E	Q	A	T	G	T	G	W	A	D	L	E	A	S	L	L	P	T	G	80
81	P	N	A	S	N	T	S	D	G	P	D	N	L	T	S	A	G	S	P	P	100
101	R	T	G	S	I	S	Y	I	N	I	I	M	P	S	V	F	G	T	I	C	120
121	L	L	G	I	I	G	N	S	T	V	I	F	A	V	V	K	K	S	K	L	140
141	H	W	C	N	N	V	P	D	I	F	I	I	N	L	S	V	V	D	L	L	160
161	F	L	E	G	M	P	F	M	I	H	Q	L	M	G	N	G	V	W	H	F	180
181	G	E	T	M	C	T	L	I	T	A	M	D	A	N	S	Q	F	T	S	T	200
201	F	I	L	T	A	M	A	I	D	R	Y	L	A	T	V	H	P	I	S	S	220
221	T	K	F	R	K	P	S	V	A	T	L	V	I	C	L	L	W	A	L	S	240
241	F	I	S	I	T	P	V	W	L	Y	A	R	L	I	P	F	P	G	G	A	260
261	V	G	C	G	I	R	L	P	N	P	D	T	D	L	Y	W	F	T	L	Y	280
281	Q	F	F	L	A	F	A	L	P	F	V	V	I	T	A	A	Y	V	R	I	300
301	L	Q	R	M	T	S	S	V	A	P	A	S	Q	R	S	I	R	L	R	T	320
321	K	R	V	T	R	T	A	I	A	I	C	L	V	F	F	V	C	W	A	P	340
341	Y	Y	V	L	Q	L	T	Q	L	S	I	S	R	P	T	L	T	F	V	Y	360
361	L	Y	N	A	A	I	S	L	G	Y	A	N	S	C	L	N	P	F	V	Y	380
381	I	V	L	C	E	T	F	R	K	R	L	V	L	S	V	K	P	A	A	Q	400
401	G	Q	L	R	A	V	S	N	A	Q	T	A	D	E	E	R	T	E	S	K	420
421	G	T																			422

10029344-10001

15/27

FIGURE 15

1	M	D	L	E	A	S	L	L	P	T	G	P	N	A	S	N	T	S	D	G	20
21	P	D	N	L	T	S	A	G	S	P	P	R	T	G	S	I	S	Y	I	N	40
41	I	I	M	P	S	V	F	G	T	I	C	L	L	G	I	I	G	N	S	T	60
61	V	I	F	A	V	V	K	K	S	K	L	H	W	C	N	N	V	P	D	I	80
81	F	I	I	N	L	S	V	V	D	L	L	F	L	L	G	M	P	F	M	I	100
101	H	Q	L	M	G	N	G	V	W	H	F	G	E	T	M	C	T	L	I	T	120
121	A	M	D	A	N	S	Q	F	T	S	T	Y	I	L	T	A	M	A	I	D	140
141	R	Y	L	A	T	V	H	P	I	S	S	T	K	F	R	K	P	S	V	A	160
161	T	L	V	I	C	L	L	W	A	L	S	F	I	S	I	T	P	V	W	L	180
181	F	A	R	L	I	P	F	P	G	G	A	V	G	C	G	I	R	L	P	N	200
201	P	D	T	D	L	Y	W	F	T	L	Y	Q	F	F	L	A	F	A	L	P	220
221	F	V	V	I	T	A	A	Y	V	R	I	L	Q	R	M	T	S	S	V	A	240
241	P	A	S	Q	R	S	I	R	L	R	T	K	R	V	T	R	T	A	I	A	260
261	I	C	L	V	F	F	V	C	W	A	P	Y	Y	V	L	Q	L	T	Q	L	280
281	S	I	S	R	F	T	L	T	F	V	Y	L	Y	N	A	A	I	S	L	G	300
301	Y	A	N	S	C	L	N	P	F	V	Y	I	V	L	C	E	T	F	R	K	320
321	R	L	V	L	S	V	K	P	A	A	Q	G	Q	L	R	A	V	S	N	A	340
341	Q	T	A	D	E	E	R	T	E	S	K	G	T								353

1002344-12001

FIGURE 16

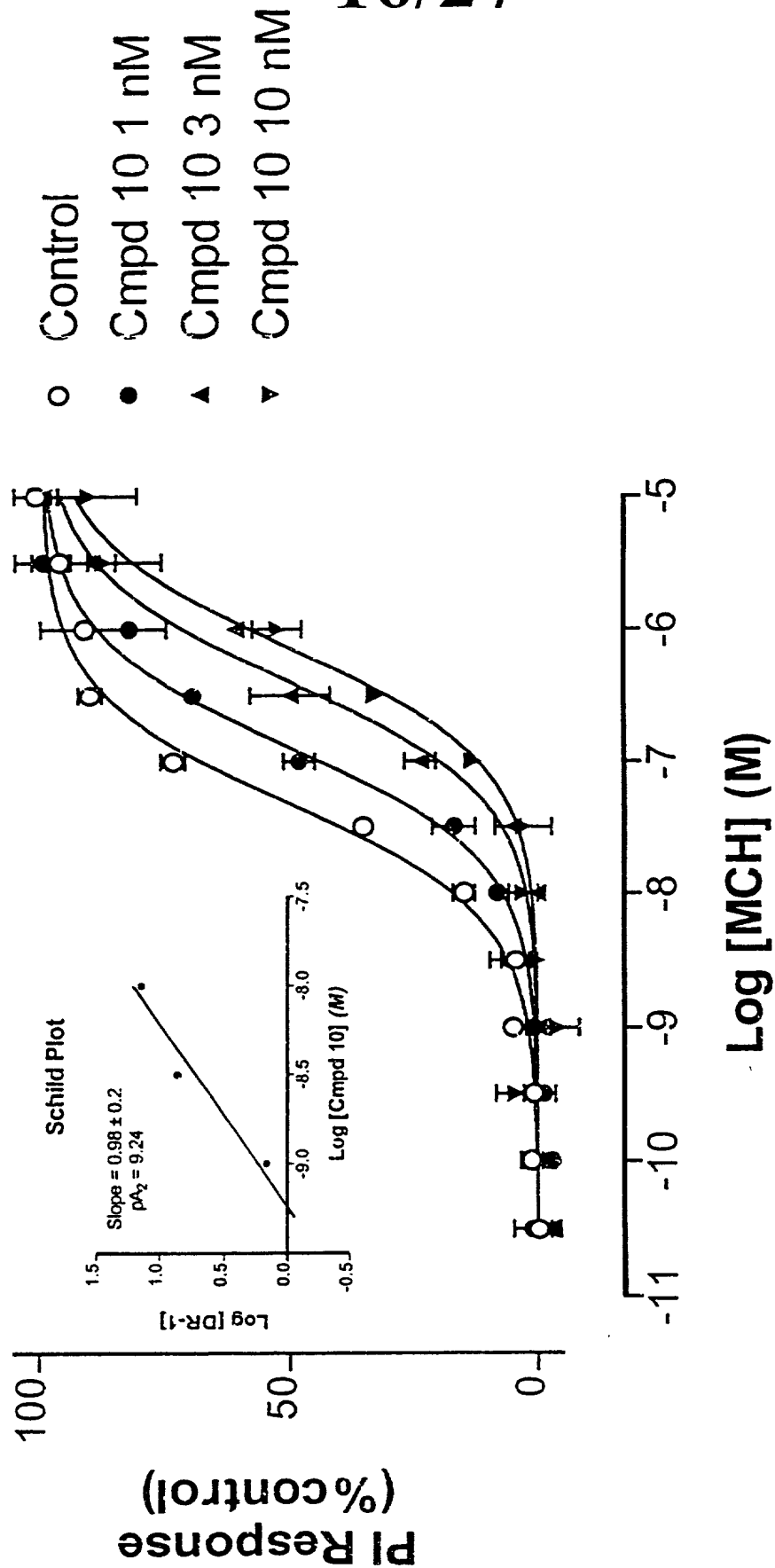


FIGURE 17

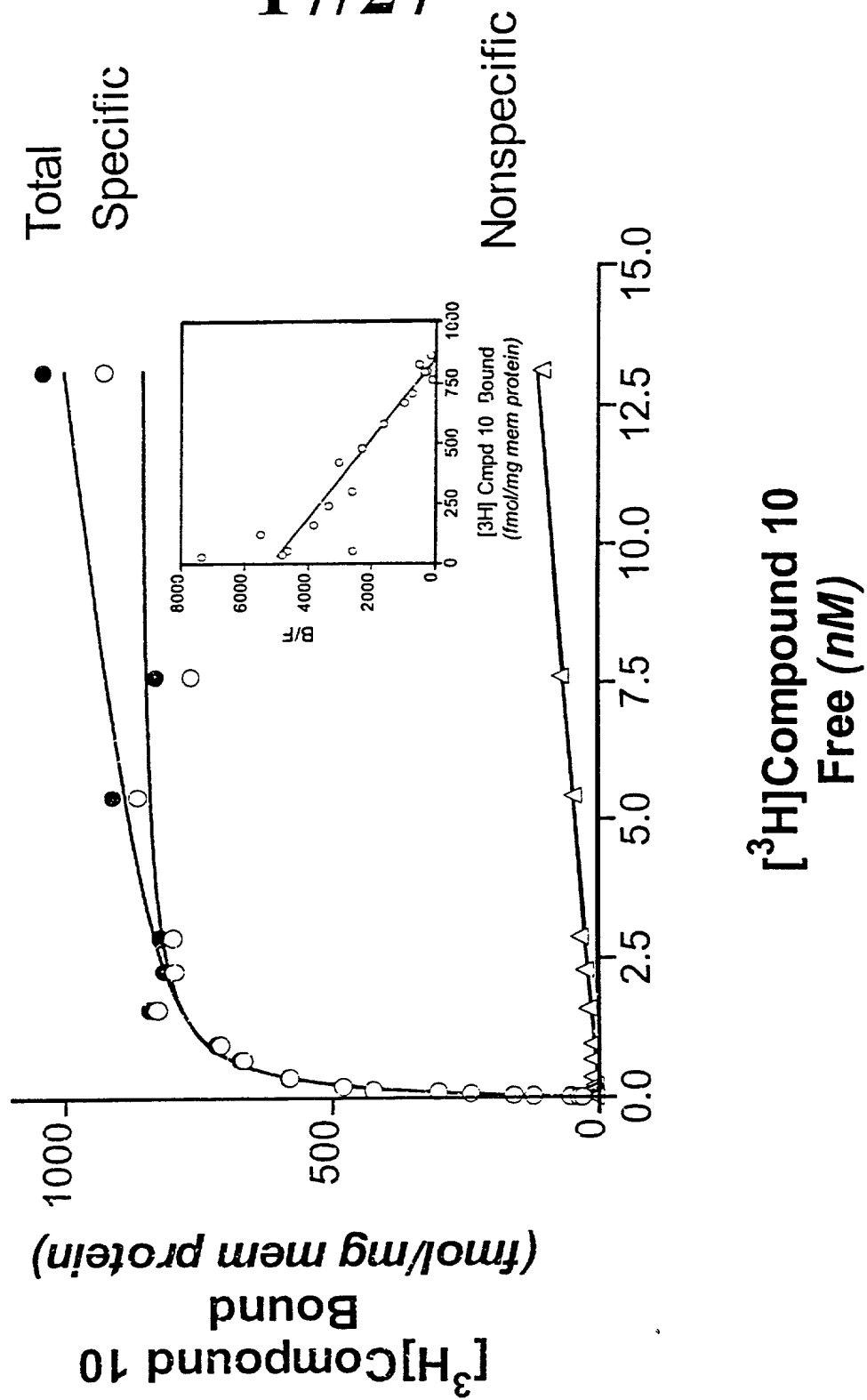
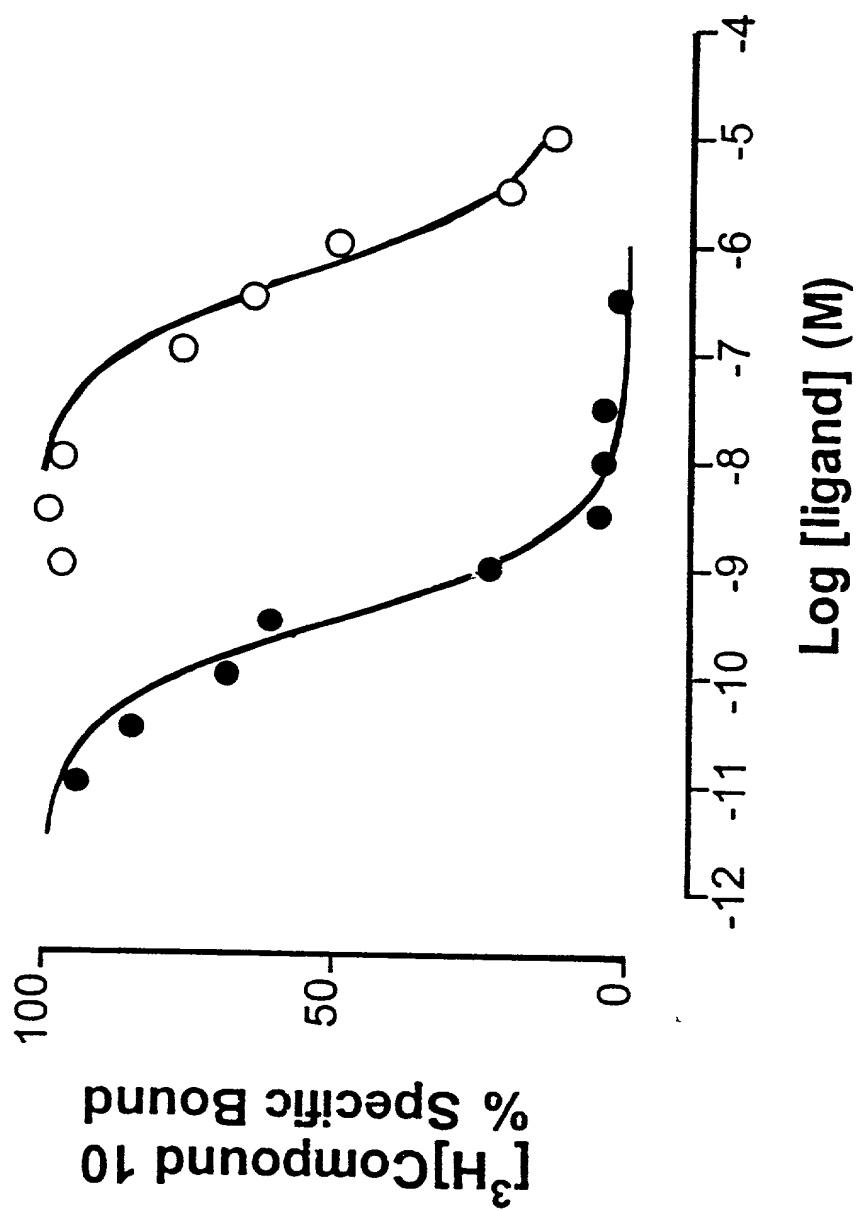


FIGURE 18



18/27

19/27

FIGURE 19

**Total MCH1
Receptor Binding**

A



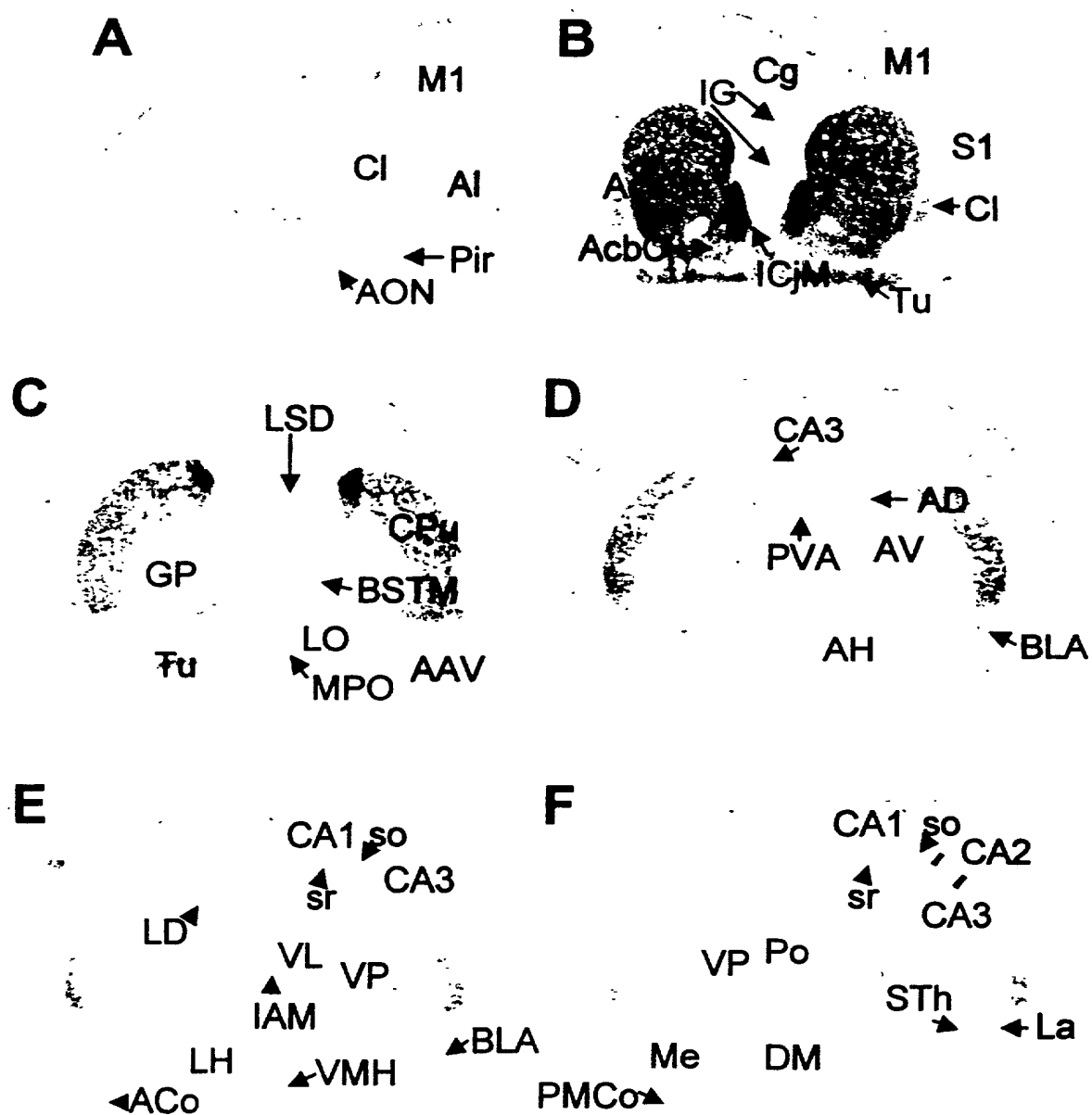
Nonspecific binding

B



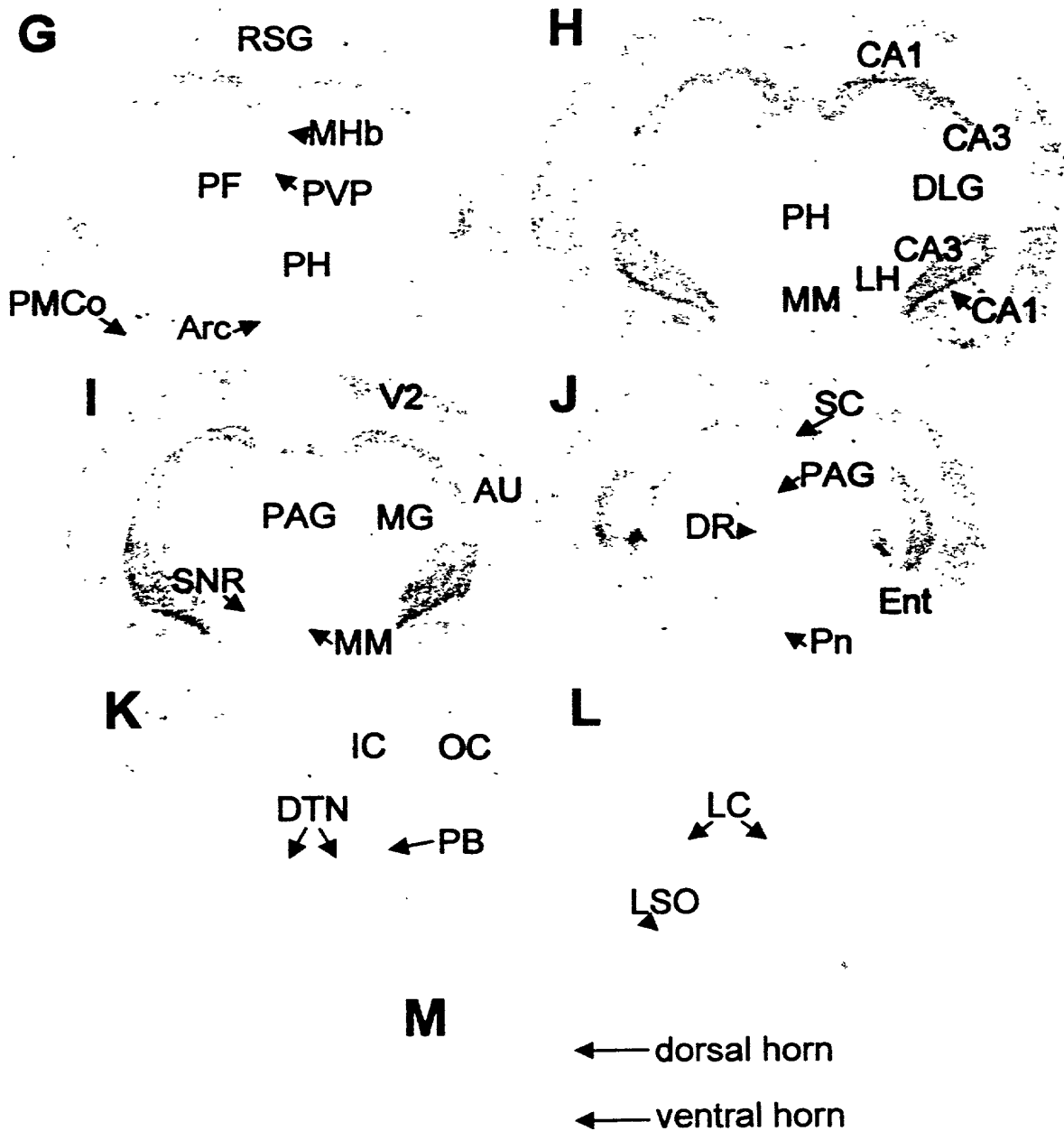
10069314-12001

FIGURE 20A



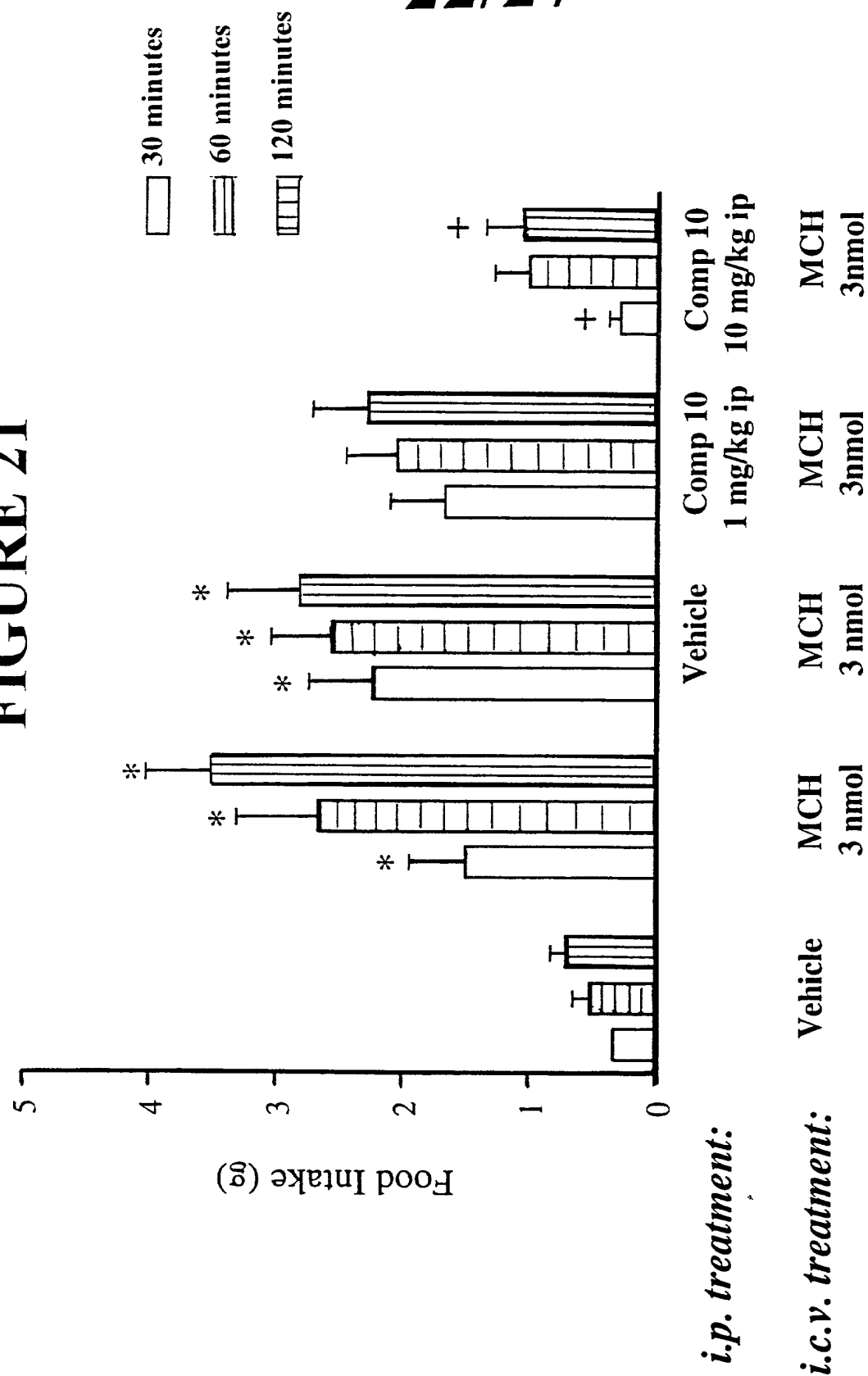
21/27

FIGURE 20B



10069344, 20001

FIGURE 21



23/27

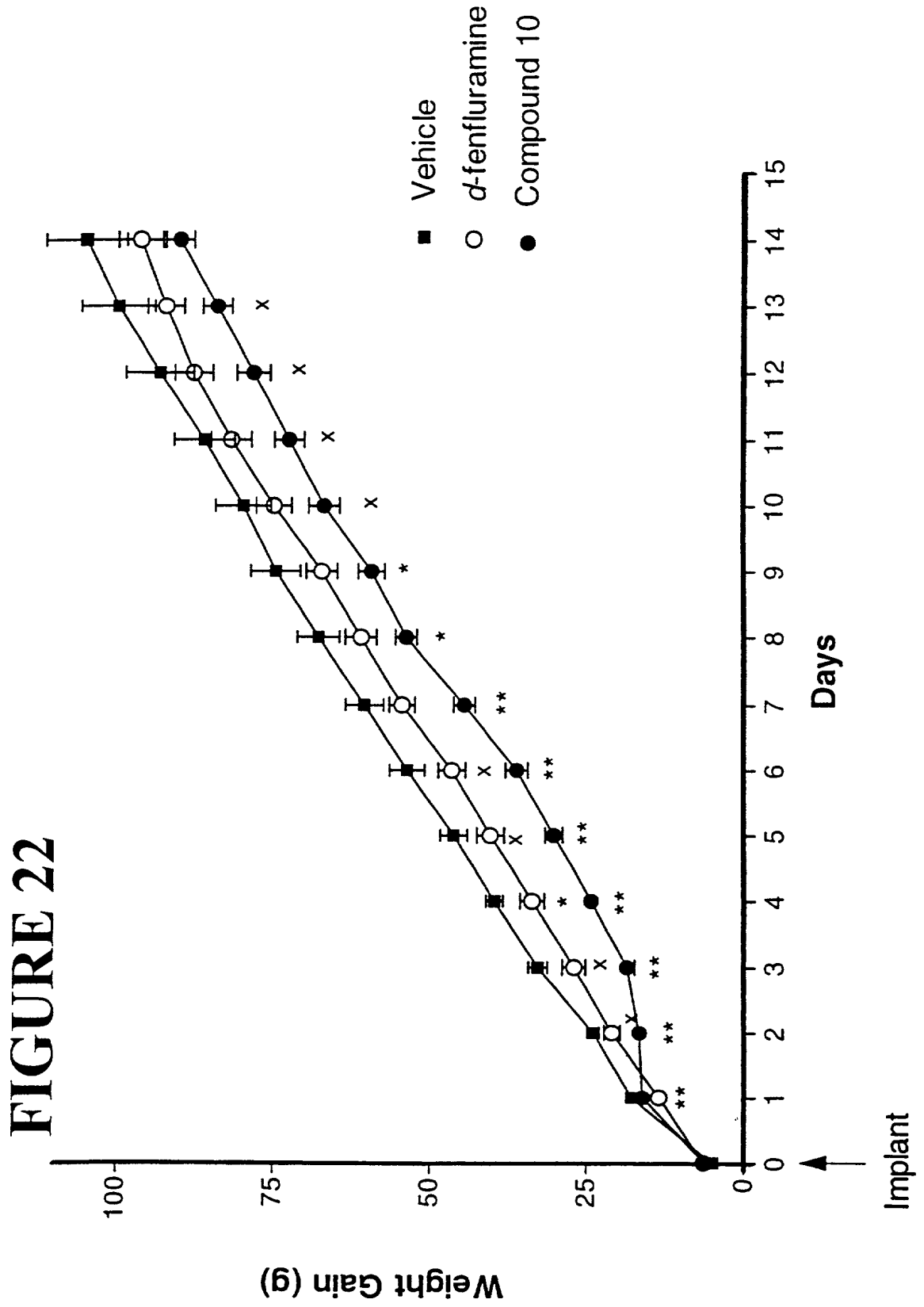
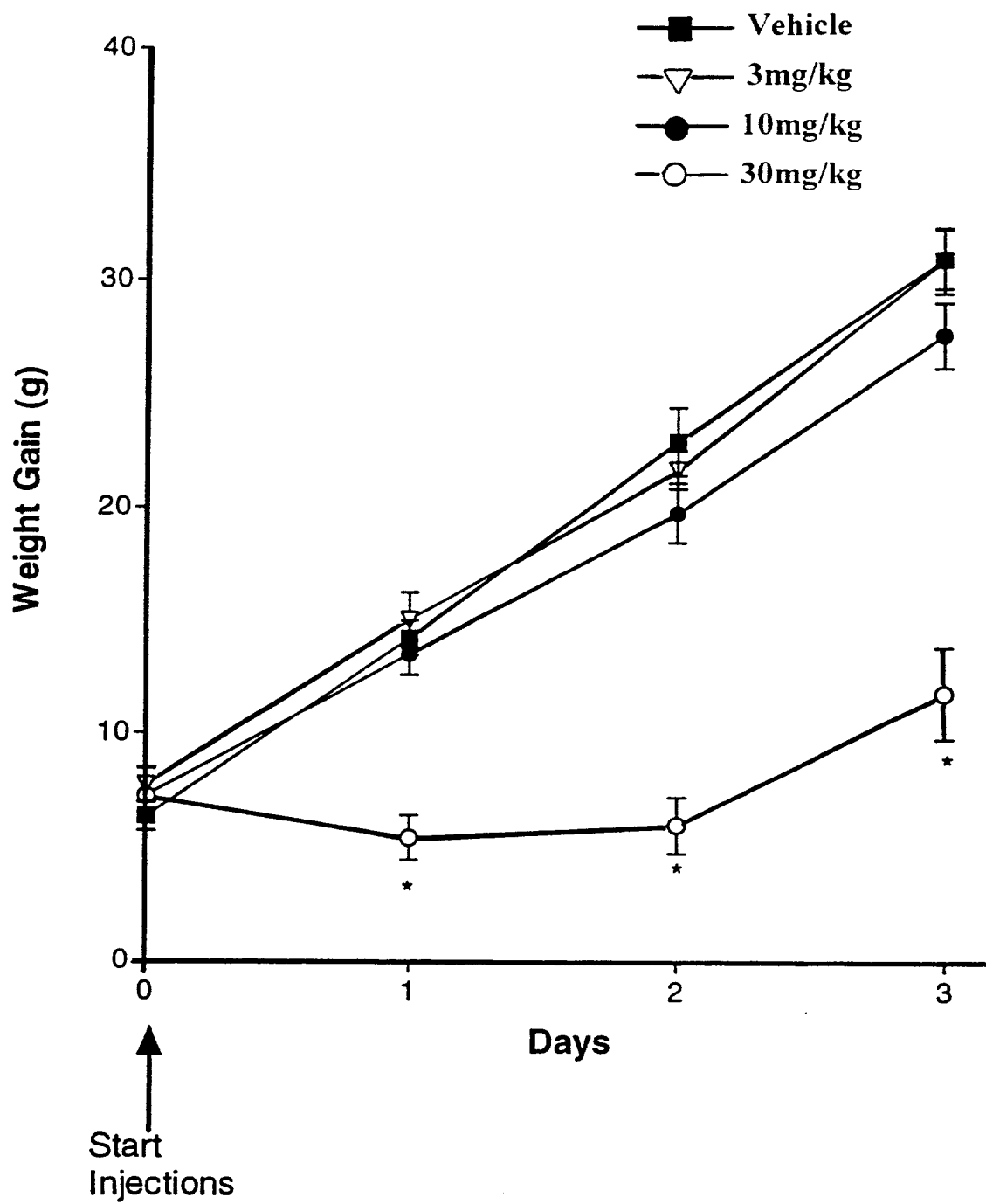
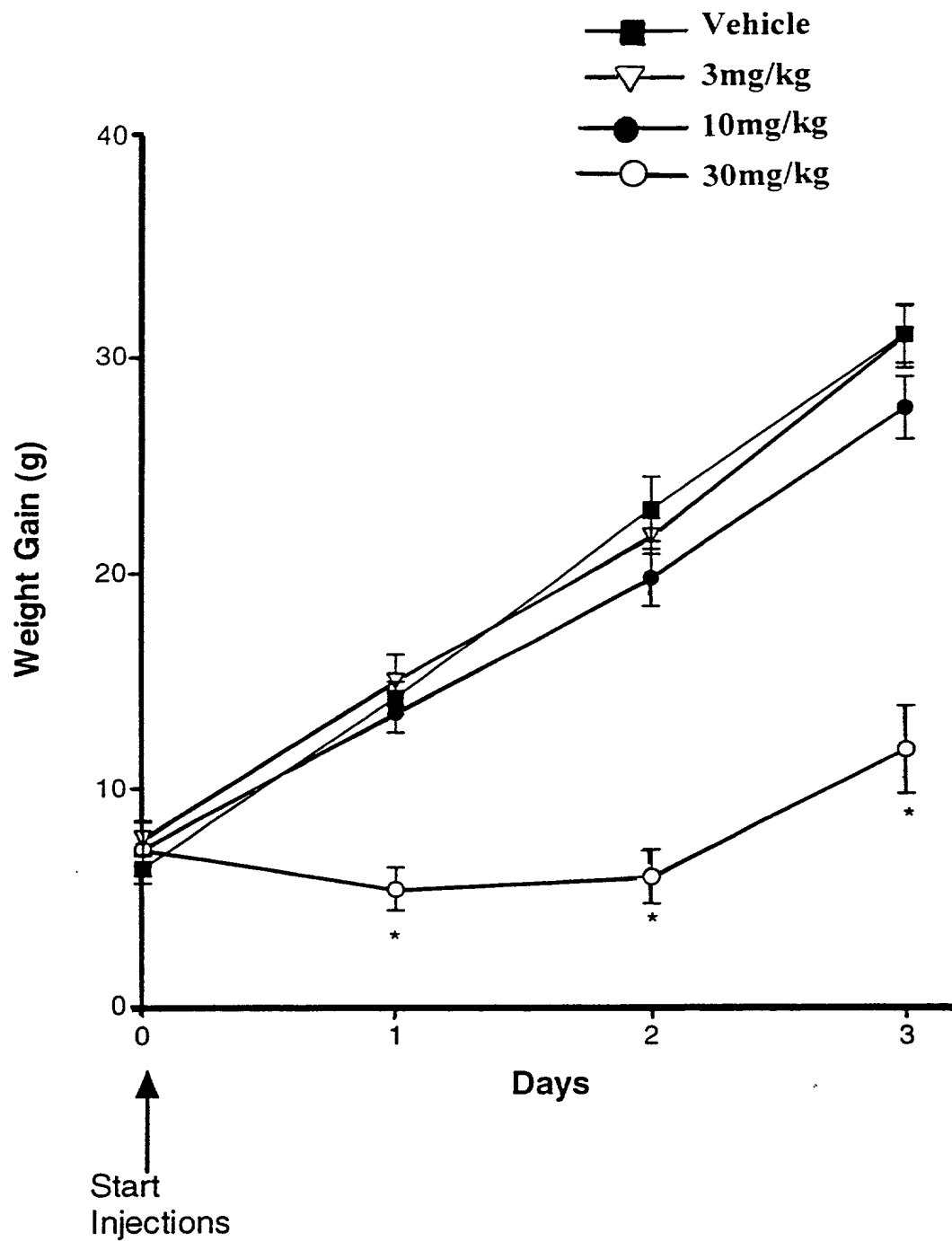


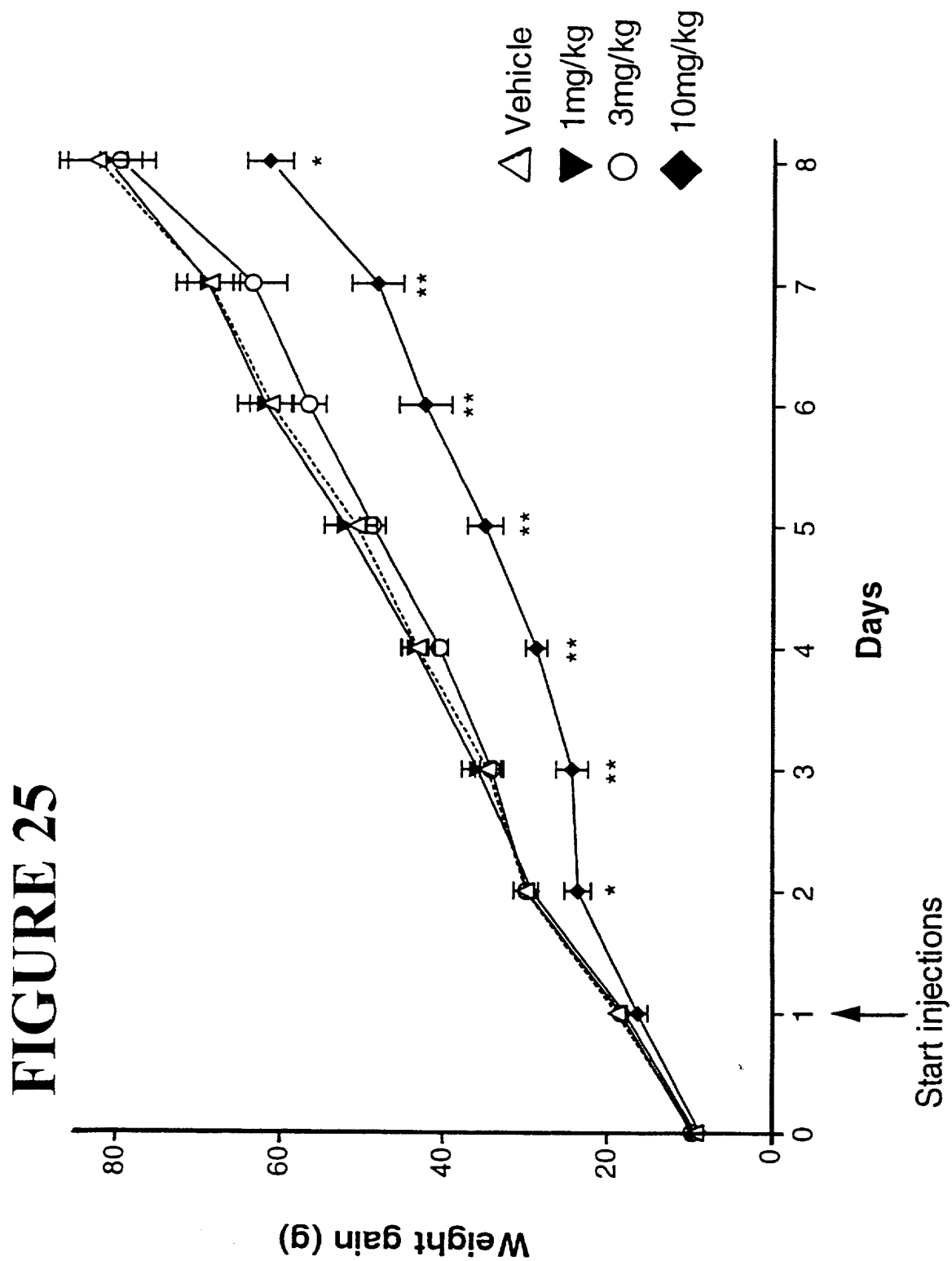
FIGURE 23



25/27

FIGURE 24





27/27

FIGURE 26

